SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Bhat, Ramesh, A.
Henderson,, Ruth
Hsiao, Chulai
Karathanasis, Sotirios

(ii) TITLE OF THE INVENTION: NOVEL HUMAN ESTROGEN RECE
PTOR-BETA

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:
  (A) ADDRESSEE: Darby & Darby, P.C.
  (B) STREET: 805 Third Avenue, 27th Floor
  (C) CITY: New York
  (D) STATE: NY
  (E) COUNTRY: USA
  (F) ZIP: 10022

(v) COMPUTER READABLE FORM:
  (A) MEDIUM TYPE: Diskette
  (B) COMPUTER: IBM Compatible
  (C) OPERATING SYSTEM: DOS
  (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
  (A) APPLICATION NUMBER: 09/429,832
  (B) FILING DATE: 29-OCT-1999
  (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
  (A) APPLICATION NUMBER: 08/906365
  (B) FILING DATE: 05- AUG-1997

(viii) ATTORNEY/AGENT INFORMATION:
  (A) NAME: Robinson, Joseph R
  (B) REGISTRATION NUMBER: 33,448
  (C) REFERENCE/DOCKET NUMBER: 0646/1D205

(ix) TELECOMMUNICATION INFORMATION:
  (A) TELEPHONE: 212-527-1700
  (B) TELEFAX: 212-753-6237
  (C) TELEX: 236687

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 1466 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

```
CAGCCATTAT ACTTGCTCAC GAATCTTTGA GAACATTATA ATGACCTTTG TGCCTCTTCT      60
TGCAAGGTGT TTTCTCAGCT GCTATCTCAA GACATGGATA TAAAAAACTC ACCATTTAGC     120
CTTAATTCTC CTTCCTCCTA CAACTGCAGT CAATCCATCT TACCTCTGGA GCACGGCTCC     180
ATATACATAC CTTCCTCCTA TGTAGACAGC CACCATGAAT ATCCAGCCAT GACATTCTAT     240
AGCCCTGCTG TGATGAATTA CAGCCATTCC AGCAATGTCA CTAACTTGCA AGGTGGGCCT     300
GGTCGGCAGA CCACAAGCCC AAATGTCTTG TGGCCAACAC CTGGGCACCT TTCTCCTTTA     360
GTGGTCCATC GCCAGTTATC ACATCTCTAT GCGGAACCTC AAAAGAGTCC CTGGTGTGAA     420
GCAAGATCGC TAGAACACAC CTTACCTGTA AACAGAGAGA CACTGAAAAG GAAGGTTAGT     480
GGGAACCGTT GCGCCAGCCC TGTTACTGGT CCAGGTTCAA AGAGGGATGC TCACTTCTGC     540
GCTGTCTGCA GCGATTACGC ATCGGGATAT CACTATGGAG TCTGGTCGTG TGAAGGATGT     600
AAGGCCTTTT TTAAAAGAAG CATTCAAGGA CATAATGATT ATATTTGTCC AGCTACAAAT     660
CAGTGTACAA TCGATAAAAA CCGGGCGCAAG AGCTGCCAGG CCTGCCGACT TCGGAAGTGT     720
TACGAAGTGG GAATGGGTGAA GTGTGGCTCC CGGAGAGAGA GATGTGGGTA CCGCCTTGTG     780
CGGAGACAGA GAAGTGCCGA CGAGCACTG CACTGTGCCG GCAAGGCCAA GAGAAGTGGC     840
GGCCACGCGC CCCGAGTGCG GGAGCTGCTG CTGGACGCCC TGAGCCCCGA GCAGCTAGTG     900
CTCACCCTCC TGGAGGCTGA GCCGGCCCAT GTGCTCGATCA GCCGCCCCAG TGCGCCCTTC     960
ACCGAGGCCT CCATGATGAT GTCCCTGACC AAGTTGGCCG ACAAGGAGTT GGTACACATG    1020
ATCAGCTGGG CCAAGAAGAT TCCCGGCTTT GTGGAGCTCA GCCTGTTCGA CCAAGTGCGG    1080
CTCTTGGAGA GCTGTTGGAT GGAGGTGTTA ATGATGGGGC TGATGTGGCG CTCAATTGAC    1140
CACCCCGGCA AGCTCATCTT TGCTCCAGAT CTTGTTCTGG ACAGGGATGA GGGGAAATGC    1200
GTAGAAGGAA TTCTGGAAAT CTTTGACATG CTCCTGGCAA CTACTTCAAG GTTTCGAGAG    1260
TTAAAACTCC AACACAAAGA ATATCTCTGT GTCAAGGCCA TGATCCTGCT CAATTCCAGT    1320
ATGTACCCTC TGGTCACAGC GACCCAGGAT GCTGACAGCA GCCGGAAGCT GGCTCACTTG    1380
CTGAACGCCG TGACCGATGC TTTGGTTTGG GTGATTGCCA AGAGCGGCAT CTCCTCCCAG    1440
CAGCAATCCA TGCGCCTGGC TAACCTCCTG ATGCTCCTGT CCCACGTCAG GCATGCGAGT    1500
AACAAGGGCA TGGAACATCT GCTCAACATG AAGTGCAAAA ATGTGGTCCC AGTGTATGAC    1560
CTGCTGCTGG AGATGCTGAA TGCCCACGTG CTTCGCGGGT GCAAGTCCTC CATCACGGGG    1620
TCCGAGTGCA GCCCGGCAGA GGACAGTAAA AGCAAAGAGG GCTCCCAGAA CCCACAGTCT    1680
CAGTGA                                                                1686
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Met Asp Ile Lys Asn Ser Pro Ser Ser Leu Asn Ser Pro Ser Ser Tyr
 1               5                  10                  15
Asn Cys Ser Gln Ser Ile Leu Pro Leu Glu His Gly Ser Ile Tyr Ile
            20                  25                  30
Pro Ser Ser Tyr Val Asp Ser His His Glu Tyr Pro Ala Met Thr Phe
            35                  40                  45
Tyr Ser Pro Ala Val Met Asn Tyr Ser Ile Pro Ser Asn Val Thr Asn
                    50                  55                  60
Leu Gln Gly Gly Pro Gly Arg Gln Thr Thr Ser Pro Asn Val Leu Trp
 65                  70                  75                  80
Pro Thr Pro Gly His Leu Ser Pro Leu Val Val His Arg Gln Leu Ser
                    85                  90                  95
His Leu Tyr Ala Glu Pro Gln Lys Ser Pro Trp Tyr Glu Ala Arg Ser
                    100                 105                 110
Leu Glu His Thr Leu Pro Val Asn Arg Glu Thr Leu Lys Arg Lys Val
            115                 120                 125
Ser Gly Asn Arg Tyr Ala Ser Pro Val Thr Gly Ile Gly Ser Lys Arg
```

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           1??                         139                          14?
Asp Ala His Phe Lys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His
145                     150                     155                 160
Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser
                    165                 170                 175
Ile Gln Gly His Asn Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr
                    180                 185                 190
Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys
                195                 200                 205
Cys Tyr Glu Val Gly Met Val Lys Cys Gly Ser Arg Arg Glu Arg Cys
            210                 215                 220
Gly Tyr Arg Leu Val Arg Arg Gln Arg Ser Ala Asp Glu Gln Leu His
225                 230                 235                 240
Cys Ala Gly Lys Ala Lys Arg Ser Gly Gly His Ala Pro Arg Val Arg
                    245                 250                 255
Glu Leu Leu Leu Asp Ala Leu Ser Pro Glu Gln Leu Val Leu Thr Leu
                260                 265                 270
Leu Glu Ala Glu Pro Pro His Val Leu Ile Ser Arg Pro Ser Ala Pro
            275                 280                 285
Phe Thr Glu Ala Ser Met Met Met Ser Leu Thr Lys Leu Ala Asp Lys
            290                 295                 300
Glu Leu Val His Met Ile Ser Trp Ala Lys Lys Ile Pro Gly Phe Val
305                 310                 315                 320
Glu Leu Ser Leu Phe Asp Gln Val Arg Leu Leu Glu Ser Cys Trp Met
                325                 330                 335
Glu Val Leu Met Met Gly Leu Met Trp Arg Ser Ile Asp His Pro Gly
            340                 345                 350
Lys Leu Ile Phe Ala Pro Asp Leu Val Leu Asp Arg Asp Glu Gly Lys
            355                 360                 365
Cys Val Glu Gly Ile Leu Glu Ile Phe Asp Met Leu Leu Ala Thr Thr
            370                 375                 380
Ser Arg Phe Arg Glu Leu Lys Leu Gln His Lys Glu Tyr Leu Cys Val
385                 390                 395                 400
Lys Ala Met Ile Leu Leu Asn Ser Ser Met Tyr Pro Leu Val Thr Ala
                405                 410                 415
Thr Gln Asp Ala Asp Ser Ser Arg Lys Leu Ala His Leu Leu Asn Ala
            420                 425                 430
Val Thr Asp Ala Leu Val Trp Val Ile Ala Lys Ser Gly Ile Ser Ser
            435                 440                 445
Gln Gln Gln Ser Met Arg Leu Ala Asn Leu Leu Met Leu Leu Ser His
            450                 455                 460
Val Arg His Ala Ser Asn Lys Gly Met Glu His Leu Leu Asn Met Lys
465                 470                 475                 480
Cys Lys Asn Val Val Pro Val Tyr Asp Leu Leu Leu Glu Met Leu Asn
                485                 490                 495
Ala His Val Leu Arg Gly Cys Lys Ser Ser Ile Thr Gly Ser Glu Cys
            500                 505                 510
Ser Pro Ala Glu Asp Ser Lys Ser Lys Glu Gly Ser Gln Asn Pro Gln
            515                 520                 525
Cys Ser
        529
```

(2) INFORMATION FOR SEQ ID NO:8:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1? amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Thr Gly Tyr Ser Pro Ala Val Met Asn Tyr Ser
1   5   10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 10 amino acids
   (B) TYPE: amino acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gly Tyr Ser Pro Ala Val Met Asn Tyr Ser
1   5   10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 45 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGAAGCTTGT CGACCATCAT GACCGGCTAT AGCCCTGCTG TGATG   45

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 40 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGATCTAGAC TCGAGCCGTC ACTGAGACTG AGGGTTCTGG   40

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 4 amino acids
   (B) TYPE: amino acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Thr Gly Tyr
1

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 14 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
  (B) CLONE: R61C10-2.24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCATCACCGG CTAT   14

    (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 23 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
  (A) ORGANISM: pOB2 sequencing primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTGGTAAGTT TAGTCTTTTT GTC   23

    (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 25 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
  (A) ORGANISM: oligo #12908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTTCACACC AAGGACTCTT TTGAG   25

    (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 26 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
  (A) ORGANISM: oligo #14871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTTGGTCA A A TCATTT TT GTTTT   26

    (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 27 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Adaptor primer 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCATCCTAAT ACGACTCACT ATAGGGC   27

    (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 0 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Nested adaptor primer 2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACTCACTATAGGGCTCGAGCGGC